



PCT

RAW SEQUENCE LISTING

DATE: 10/11/2005

PATENT APPLICATION: US/10/549,871

TIME: 11:35:45

Input Set : N:\Cr4\10042005\J459871.raw

Output Set: N:\CRF4\10062005\J549871.raw

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1 <110> APPLICANT: Kunkel, Andreas
2      Veen, Markus
3      Lang, Christine
4 <120> TITLE OF INVENTION: Method for producing ergosta-5,7-dienol and/or biosynthetic
5      intermediate and/or secondary products thereof in transgenic
6      organisms
7 <130> FILE REFERENCE: 12810-00126-US
8 <140> CURRENT APPLICATION NUMBER: US/10/549,871
9 <141> CURRENT FILING DATE: 2005-09-16
10 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/002582
11 <151> PRIOR FILING DATE: 2004-03-12
12 <150> PRIOR APPLICATION NUMBER: DE 103 12 314.8
13 <151> PRIOR FILING DATE: 2003-03-19
14 <160> NUMBER OF SEQ ID NOS: 14
15 <170> SOFTWARE: PatentIn version 3.3
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1617
19 <212> TYPE: DNA
20 <213> ORGANISM: Saccharomyces cerevisiae
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (1)..(1617)
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26      Met Ser Ser Val Ala Glu Asn Ile Ile Gln His Ala Thr His Asn Ser
27      1          5          10          15
28      acg cta cac caa ttg gct aaa gac cag ccc tct gta ggc gtc act act      96
29      Thr Leu His Gln Leu Ala Lys Asp Gln Pro Ser Val Gly Val Thr Thr
30      20          25          30
31      gcc ttc agt atc ctg gat aca ctt aag tct atg tca tat ttg aaa ata      144
32      Ala Phe Ser Ile Leu Asp Thr Leu Lys Ser Met Ser Tyr Leu Lys Ile
33      35          40          45
34      ttt gct act tta atc tgt att ctt ttg gtt tgg gac caa gtt gca tat      192
35      Phe Ala Thr Leu Ile Cys Ile Leu Leu Val Trp Asp Gln Val Ala Tyr
36      50          55          60
37      caa atc aag aaa ggt tcc atc gca ggt cca aag ttt aag ttc tgg ccc      240
38      Gln Ile Lys Lys Gly Ser Ile Ala Gly Pro Lys Phe Lys Phe Trp Pro
39      65          70          75          80
40      atc atc ggt cca ttt ttg gaa tcc tta gat cca aag ttt gaa gaa tat      288
41      Ile Ile Gly Pro Phe Leu Glu Ser Leu Asp Pro Lys Phe Glu Glu Tyr
42      85          90          95
43      aag gct aag tgg gca tcc ggt cca ctt tca tgt gtt tct att ttc cat      336
44      Lys Ala Lys Trp Ala Ser Gly Pro Leu Ser Cys Val Ser Ile Phe His

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Input Set : N:\Cr4\10042005\J459871.raw

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45		100		105		110	
46	aaa ttt gtt gtt atc gca tct act aga gac ttg gca aga aag atc ttg						384
47	Lys Phe Val Val Ile Ala Ser Thr Arg Asp Leu Ala Arg Lys Ile Leu						
48		115		120		125	
49	caa tct tcc aaa ttc gtc aaa cct tgc gtt gtc gat gtt gct gtg aag						432
50	Gln Ser Ser Lys Phe Val Lys Pro Cys Val Val Asp Val Ala Val Lys						
51		130		135		140	
52	atc tta aga cct tgc aat tgg gtt ttt ttg gac ggt aaa gct cat act						480
53	Ile Leu Arg Pro Cys Asn Trp Val Phe Leu Asp Gly Lys Ala His Thr						
54		145		150		155	160
55	gat tac aga aaa tca tta aac ggt ctt ttc act aaa caa gct ttg gct						528
56	Asp Tyr Arg Lys Ser Leu Asn Gly Leu Phe Thr Lys Gln Ala Leu Ala						
57		165		170		175	
58	caa tac tta cct tca ttg gaa caa atc atg gat aag tac atg gat aag						576
59	Gln Tyr Leu Pro Ser Leu Glu Gln Ile Met Asp Lys Tyr Met Asp Lys						
60		180		185		190	
61	ttt gtt cgt tta tct aag gag aat aac tac gag ccc cag gtc ttt ttc						624
62	Phe Val Arg Leu Ser Lys Glu Asn Asn Tyr Glu Pro Gln Val Phe Phe						
63		195		200		205	
64	cat gaa atg aga gaa att ctt tgc gcc tta tca ttg aac tct ttc tgt						672
65	His Glu Met Arg Glu Ile Leu Cys Ala Leu Ser Leu Asn Ser Phe Cys						
66		210		215		220	
67	ggt aac tat att acc gaa gat caa gtc aga aag att gct gat gat tac						720
68	Gly Asn Tyr Ile Thr Glu Asp Gln Val Arg Lys Ile Ala Asp Asp Tyr						
69		225		230		235	240
70	tat ttg gtt aca gca gca ttg gaa tta gtc aac ttc cca att att atc						768
71	Tyr Leu Val Thr Ala Ala Leu Glu Leu Val Asn Phe Pro Ile Ile Ile						
72		245		250		255	
73	cct tac act aaa aca tgg tat ggt aag aaa act gca gac atg gcc atg						816
74	Pro Tyr Thr Lys Thr Trp Tyr Gly Lys Lys Thr Ala Asp Met Ala Met						
75		260		265		270	
76	aag att ttc gaa aac tgt gct caa atg gct aag gat cat att gct gca						864
77	Lys Ile Phe Glu Asn Cys Ala Gln Met Ala Lys Asp His Ile Ala Ala						
78		275		280		285	
79	ggt ggt aag cca gtt tgt gtt atg gat gct tgg tgt aag ttg atg cac						912
80	Gly Gly Lys Pro Val Cys Val Met Asp Ala Trp Cys Lys Leu Met His						
81		290		295		300	
82	gat gca aag aat agt aac gat gat gat tct aga atc tac cac aga gag						960
83	Asp Ala Lys Asn Ser Asn Asp Asp Asp Ser Arg Ile Tyr His Arg Glu						
84		305		310		315	320
85	ttt act aac aag gaa atc tcc gaa gct gtt ttc act ttc tta ttt gct						1008
86	Phe Thr Asn Lys Glu Ile Ser Glu Ala Val Phe Thr Phe Leu Phe Ala						
87		325		330		335	
88	tct caa gat gcc tct tct tct tta gct tgt tgg ttg ttc caa att gtt						1056
89	Ser Gln Asp Ala Ser Ser Ser Leu Ala Cys Trp Leu Phe Gln Ile Val						
90		340		345		350	
91	gct gac cgt cca gat gtc tta gct aag atc aga gaa gaa caa ttg gct						1104
92	Ala Asp Arg Pro Asp Val Leu Ala Lys Ile Arg Glu Glu Gln Leu Ala						
93		355		360		365	

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94      gtt cgt aac aat gac atg tct acc gaa ttg aac ttg gat ttg att gag      1152
95      Val Arg Asn Asn Asp Met Ser Thr Glu Leu Asn Leu Asp Leu Ile Glu
96      370                               375                               380
97      aaa atg aag tac acc aat atg gtc ata aaa gaa act ttg cgt tac aga      1200
98      Lys Met Lys Tyr Thr Asn Met Val Ile Lys Glu Thr Leu Arg Tyr Arg
99      385                               390                               395                               400
100     cct cct gtc ttg atg gtt cca tat gtt gtt aag aag aat ttc cca gtt      1248
101     Pro Pro Val Leu Met Val Pro Tyr Val Val Lys Lys Asn Phe Pro Val
102     405                               410                               415
103     tcc cct aac tat acc gca cca aag ggc gct atg tta att cca acc tta      1296
104     Ser Pro Asn Tyr Thr Ala Pro Lys Gly Ala Met Leu Ile Pro Thr Leu
105     420                               425                               430
106     tac cca gct tta cat gat cct gaa gtt tac gaa aat cct gat gag ttc      1344
107     Tyr Pro Ala Leu His Asp Pro Glu Val Tyr Glu Asn Pro Asp Glu Phe
108     435                               440                               445
109     atc cct gaa aga tgg gta gaa ggc tct aag gct agt gaa gca aag aag      1392
110     Ile Pro Glu Arg Trp Val Glu Gly Ser Lys Ala Ser Glu Ala Lys Lys
111     450                               455                               460
112     aat tgg ttg gtt ttt ggt tgt ggt cca cac gtt tgc tta ggt caa aca      1440
113     Asn Trp Leu Val Phe Gly Cys Gly Pro His Val Cys Leu Gly Gln Thr
114     465                               470                               475                               480
115     tat gtc atg att acc ttc gcc gct ttg ttg ggt aaa ttt gca cta tat      1488
116     Tyr Val Met Ile Thr Phe Ala Ala Leu Leu Gly Lys Phe Ala Leu Tyr
117     485                               490                               495
118     act gat ttc cat cat aca gtg act cca tta agt gaa aaa atc aag gtt      1536
119     Thr Asp Phe His His Thr Val Thr Pro Leu Ser Glu Lys Ile Lys Val
120     500                               505                               510
121     ttc gct aca att ttc cca aaa gat gat ttg tta ctg act ttc aaa aag      1584
122     Phe Ala Thr Ile Phe Pro Lys Asp Asp Leu Leu Leu Thr Phe Lys Lys
123     515                               520                               525
124     aga gac cca att act gga gaa gtc ttc gaa taa      1617
125     Arg Asp Pro Ile Thr Gly Glu Val Phe Glu
126     530                               535
128 <210> SEQ ID NO: 2
129 <211> LENGTH: 538
130 <212> TYPE: PRT
131 <213> ORGANISM: Saccharomyces cerevisiae
132 <400> SEQUENCE: 2
133     Met Ser Ser Val Ala Glu Asn Ile Ile Gln His Ala Thr His Asn Ser
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135     Thr Leu His Gln Leu Ala Lys Asp Gln Pro Ser Val Gly Val Thr Thr
136     20                               25                               30
137     Ala Phe Ser Ile Leu Asp Thr Leu Lys Ser Met Ser Tyr Leu Lys Ile
138     35                               40                               45
139     Phe Ala Thr Leu Ile Cys Ile Leu Leu Val Trp Asp Gln Val Ala Tyr
140     50                               55                               60
141     Gln Ile Lys Lys Gly Ser Ile Ala Gly Pro Lys Phe Lys Phe Trp Pro
142     65                               70                               75                               80
143     Ile Ile Gly Pro Phe Leu Glu Ser Leu Asp Pro Lys Phe Glu Glu Tyr

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144				85				90				95					
145	Lys	Ala	Lys	Trp	Ala	Ser	Gly	Pro	Leu	Ser	Cys	Val	Ser	Ile	Phe	His	
146				100					105				110				
147	Lys	Phe	Val	Val	Ile	Ala	Ser	Thr	Arg	Asp	Leu	Ala	Arg	Lys	Ile	Leu	
148				115				120					125				
149	Gln	Ser	Ser	Lys	Phe	Val	Lys	Pro	Cys	Val	Val	Asp	Val	Ala	Val	Lys	
150				130				135				140					
151	Ile	Leu	Arg	Pro	Cys	Asn	Trp	Val	Phe	Leu	Asp	Gly	Lys	Ala	His	Thr	
152							150					155				160	
153	Asp	Tyr	Arg	Lys	Ser	Leu	Asn	Gly	Leu	Phe	Thr	Lys	Gln	Ala	Leu	Ala	
154							165					170				175	
155	Gln	Tyr	Leu	Pro	Ser	Leu	Glu	Gln	Ile	Met	Asp	Lys	Tyr	Met	Asp	Lys	
156				180											190		
157	Phe	Val	Arg	Leu	Ser	Lys	Glu	Asn	Asn	Tyr	Glu	Pro	Gln	Val	Phe	Phe	
158				195				200					205				
159	His	Glu	Met	Arg	Glu	Ile	Leu	Cys	Ala	Leu	Ser	Leu	Asn	Ser	Phe	Cys	
160				210				215				220					
161	Gly	Asn	Tyr	Ile	Thr	Glu	Asp	Gln	Val	Arg	Lys	Ile	Ala	Asp	Asp	Tyr	
162							230					235				240	
163	Tyr	Leu	Val	Thr	Ala	Ala	Leu	Glu	Leu	Val	Asn	Phe	Pro	Ile	Ile	Ile	
164							245					250				255	
165	Pro	Tyr	Thr	Lys	Thr	Trp	Tyr	Gly	Lys	Lys	Thr	Ala	Asp	Met	Ala	Met	
166				260								265				270	
167	Lys	Ile	Phe	Glu	Asn	Cys	Ala	Gln	Met	Ala	Lys	Asp	His	Ile	Ala	Ala	
168				275				280					285				
169	Gly	Gly	Lys	Pro	Val	Cys	Val	Met	Asp	Ala	Trp	Cys	Lys	Leu	Met	His	
170				290				295				300					
171	Asp	Ala	Lys	Asn	Ser	Asn	Asp	Asp	Asp	Ser	Arg	Ile	Tyr	His	Arg	Glu	
172							310					315				320	
173	Phe	Thr	Asn	Lys	Glu	Ile	Ser	Glu	Ala	Val	Phe	Thr	Phe	Leu	Phe	Ala	
174							325					330				335	
175	Ser	Gln	Asp	Ala	Ser	Ser	Ser	Leu	Ala	Cys	Trp	Leu	Phe	Gln	Ile	Val	
176				340								345				350	
177	Ala	Asp	Arg	Pro	Asp	Val	Leu	Ala	Lys	Ile	Arg	Glu	Glu	Gln	Leu	Ala	
178				355								360				365	
179	Val	Arg	Asn	Asn	Asp	Met	Ser	Thr	Glu	Leu	Asn	Leu	Asp	Leu	Ile	Glu	
180				370				375				380					
181	Lys	Met	Lys	Tyr	Thr	Asn	Met	Val	Ile	Lys	Glu	Thr	Leu	Arg	Tyr	Arg	
182							390					395				400	
183	Pro	Pro	Val	Leu	Met	Val	Pro	Tyr	Val	Val	Lys	Lys	Asn	Phe	Pro	Val	
184							405					410				415	
185	Ser	Pro	Asn	Tyr	Thr	Ala	Pro	Lys	Gly	Ala	Met	Leu	Ile	Pro	Thr	Leu	
186				420								425				430	
187	Tyr	Pro	Ala	Leu	His	Asp	Pro	Glu	Val	Tyr	Glu	Asn	Pro	Asp	Glu	Phe	
188				435								440				445	
189	Ile	Pro	Glu	Arg	Trp	Val	Glu	Gly	Ser	Lys	Ala	Ser	Glu	Ala	Lys	Lys	
190				450				455				460					
191	Asn	Trp	Leu	Val	Phe	Gly	Cys	Gly	Pro	His	Val	Cys	Leu	Gly	Gln	Thr	
192							470					475				480	

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193   Tyr Val Met Ile Thr Phe Ala Ala Leu Leu Gly Lys Phe Ala Leu Tyr
194               485                      490                      495
195   Thr Asp Phe His His Thr Val Thr Pro Leu Ser Glu Lys Ile Lys Val
196               500                      505                      510
197   Phe Ala Thr Ile Phe Pro Lys Asp Asp Leu Leu Leu Thr Phe Lys Lys
198               515                      520                      525
199   Arg Asp Pro Ile Thr Gly Glu Val Phe Glu
200       530                      535
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203 <211> LENGTH: 1578
204 <212> TYPE: DNA
205 <213> ORGANISM: Artificial sequence
206 <220> FEATURE:
207 <223> OTHER INFORMATION: Description of synthetic sequence: truncated HMG
208 <220> FEATURE:
209 <221> NAME/KEY: misc_feature
210 <222> LOCATION: (1)..(1578)
211 <223> OTHER INFORMATION: CDS
212 <400> SEQUENCE: 3
213   atg gac caa ttg gtg aaa act gaa gtc acc aag aag tct ttt act gct      48
214   Met Asp Gln Leu Val Lys Thr Glu Val Thr Lys Lys Ser Phe Thr Ala
215   1               5                      10                      15
216   cct gta caa aag gct tct aca cca gtt tta acc aat aaa aca gtc att      96
217   Pro Val Gln Lys Ala Ser Thr Pro Val Leu Thr Asn Lys Thr Val Ile
218               20                      25                      30
219   tct gga tcg aaa gtc aaa agt tta tca tct gcg caa tcg agc tca tca      144
220   Ser Gly Ser Lys Val Lys Ser Leu Ser Ser Ala Gln Ser Ser Ser Ser
221               35                      40                      45
222   gga cct tca tca tct agt gag gaa gat gat tcc cgc gat att gaa agc      192
223   Gly Pro Ser Ser Ser Ser Glu Glu Asp Asp Ser Arg Asp Ile Glu Ser
224       50                      55                      60
225   ttg gat aag aaa ata cgt cct tta gaa gaa tta gaa gca tta tta agt      240
226   Leu Asp Lys Lys Ile Arg Pro Leu Glu Glu Leu Glu Ala Leu Leu Ser
227   65               70                      75                      80
228   agt gga aat aca aaa caa ttg aag aac aaa gag gtc gct gcc ttg gtt      288
229   Ser Gly Asn Thr Lys Gln Leu Lys Asn Lys Glu Val Ala Ala Leu Val
230               85                      90                      95
231   att cac ggt aag tta cct ttg tac gct ttg gag aaa aaa tta ggt gat      336
232   Ile His Gly Lys Leu Pro Leu Tyr Ala Leu Glu Lys Lys Leu Gly Asp
233               100                      105                      110
234   act acg aga gcg gtt gcg gta cgt agg aag gct ctt tca att ttg gca      384
235   Thr Thr Arg Ala Val Ala Val Arg Arg Lys Ala Leu Ser Ile Leu Ala
236       115                      120                      125
237   gaa gct cct gta tta gca tct gat cgt tta cca tat aaa aat tat gac      432
238   Glu Ala Pro Val Leu Ala Ser Asp Arg Leu Pro Tyr Lys Asn Tyr Asp
239       130                      135                      140
240   tac gac cgc gta ttt ggc gct tgt tgt gaa aat gtt ata ggt tac atg      480
241   Tyr Asp Arg Val Phe Gly Ala Cys Cys Glu Asn Val Ile Gly Tyr Met
242   145                      150                      155                      160

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RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 10/11/2005

PATENT APPLICATION: US/10/549,871

TIME: 11:35:46

Input Set : N:\Crf4\10042005\J459871.raw

Output Set: N:\CRF4\10062005\J549871.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 4

VERIFICATION SUMMARY

DATE: 10/11/2005

PATENT APPLICATION: US/10/549,871

TIME: 11:35:46

Input Set : N:\Crf4\10042005\J459871.raw

Output Set: N:\CRF4\10062005\J549871.raw

STATISTICS SUMMARY

PATENT APPLICATION: US/10/549,871

DATE: 10/11/2005

TIME: 11:35:46

Input Set : N:\Crf4\10042005\J459871.raw

Output Set: N:\CRF4\10062005\J549871.raw

Application Serial Number: US/10/549,871

Alpha or Numeric or Xml: Numeric

Application Class:

Application File Date: 09-16-2005

Art Unit: PCT

Software Application: PatentIN3.3

Total Number of Sequences: 14

Total Nucleotides: 7803

Total Amino Acids: 2533

Number of Errors: 0

Number of Warnings: 0

Number of Corrections: 0

MESSAGE SUMMARY